



SEQUENCE LISTING

#6

<110> Fernandez, Elma
Vernet, Corine
Shimkets, Richard A.

<120> Novel Human Proteins and Polynucleotides Encoding Them

<130> Cura-46 (15966-546)

<140> USSN 09/544,511

<141> 2000-04-06

<150> USSN 60/128,514

<151> 1999-04-09

<160> 57

<170> PatentIn Ver. 2.0

<210> 1

<211> 1107

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (65)..(598)

<400> 1

aattcggtac gaggtctgggg ttcaggcgagg cagcagctgc aggtctgacct tgcagcttgg 60

cgga atg gac tgg cct cac aac ctg ctg ttt ctt ctt acc att tcc atc 109
Met Asp Trp Pro His Asn Leu Leu Phe Leu Leu Thr Ile Ser Ile
1 5 10 15

ttc ctg ggg ctg ggc agc cag gag ccc caa aag caa gag gaa ggg gca 157
Phe Leu Gly Leu Gly Ser Gln Glu Pro Gln Lys Gln Glu Glu Gly Ala
20 25 30

agg gcg gcc tgg gcc ctg gcc tgg cct cac cag gtg cca ctg gac ctg 205
Arg Ala Ala Trp Ala Leu Ala Trp Pro His Gln Val Pro Leu Asp Leu
35 40 45

gtg tca cgg atg aaa ccg tat gcc cgc atg gag gag tat gag agg aac 253
Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg Asn
50 55 60

atc gag gag atg gtg gcc cag ctg aggaac agc tca gag ctg gcc cag	301
Ile Glu Glu Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala Gln	
65 70 75	
aga aag tgt gag gtc aac ttg cag ctg tgg atg tcc aac aag agg agc	349
Arg Lys Cys Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg Ser	
80 85 90 95	
ctg tct ccc tgg ggc tac agc atc aac cac gac ccc agc cgt atc ccc	397
Leu Ser Pro Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile Pro	
100 105 110	
gtg gac ctg ccg gag gca cgg tgc ctg tgt ctg ggc tgt gtg aac ccc	445
Val Asp Leu Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn Pro	
115 120 125	
ttc acc atg cag gag gac cgc agc atg gtg agc gtg ccg gtg ttc agc	493
Phe Thr Met Gln Glu Asp Arg Ser Met Val Ser Val Pro Val Phe Ser	
130 135 140	
cag gtt cct gtg cgc cgc cgc ctc tgc ccg cca ccg ccc cgc aca ggg	541
Gln Val Pro Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly	
145 150 155	
cct tgc cgc cag cgc gca gtc atg gag acc atc gct gtg ggc tgc acc	589
Pro Cys Arg Gln Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr	
160 165 170 175	
tgc atc ttc tgaatcacct ggcccagaag ccaggccagc agcccagac	638
Cys Ile Phe	
catcctcctt gcacctttgt gccaaagaaag gcctatgaaa agtaaacact gacttttgaa	698
agcaaaaaaaaaa cccaggaag cttcggctgg gttccagaca catggaaaac agacttcctg	758
tgccagcgca tgctgatccc ttcagcagcc gcttctccac ccttggggct gctctccagc	818
acctggcagt gtccagagcg gatagggggc cctgttttgg tgaatgagtg cacagacgcc	878
tctaggggga gcccaagatc tgctcctgc ctccctctat tatgccttca taggtgggtc	938
agaacaaaga attccttata aacctcccg gtccccact gccaatcacc cacctccatt	998
ctaccctcta cagctgcccc ttatcccca agtcttgaa attttgcttg ggtcacctgc	1058
tccaggaggc agagttccca tgaagggtat taaacgtcta ctacactgc	1107

Asn	Ile	Ser	Leu	Thr	Cys	Ile	Ala	Thr	Gly	Arg	Pro	Glu	Pro	Thr	Val		
			155						160						165		
act	tgg	aga	cac	atc	tct	ccc	aaa	gcg	gtt	ggc	ttt	gtg	agt	gaa	gac	640	
Thr	Trp	Arg	His	Ile	Ser	Pro	Lys	Ala	Val	Gly	Phe	Val	Ser	Glu	Asp		
			170						175						180		
gaa	tac	ttg	gaa	att	cag	ggc	atc	acc	cgg	gag	cag	tca	ggg	gac	tac	688	
Glu	Tyr	Leu	Glu	Ile	Gln	Gly	Ile	Thr	Arg	Glu	Gln	Ser	Gly	Asp	Tyr		
			185						190						195		
gag	tgc	agt	gcc	tcc	aat	gac	gtg	gcc	gcg	ccc	gtg	gta	cgg	aga	gta	736	
Glu	Cys	Ser	Ala	Ser	Asn	Asp	Val	Ala	Ala	Pro	Val	Val	Arg	Arg	Val		
			200						205						210		
aag	gtc	acc	gtg	aac	tat	cca	cca	tac	att	tca	gaa	gcc	aag	ggg	aca	784	
Lys	Val	Thr	Val	Asn	Tyr	Pro	Pro	Tyr	Ile	Ser	Glu	Ala	Lys	Gly	Thr		
			220						225						230		
ggg	gtc	ccc	gtg	gga	caa	aag	ggg	aca	ctg	cag	tgt	gaa	gcc	tca	gca	832	
Gly	Val	Pro	Val	Gly	Gln	Lys	Gly	Thr	Leu	Gln	Cys	Glu	Ala	Ser	Ala		
			235						240						245		
gtc	ccc	tca	gca	gaa	ttc	cag	tgg	tac	aag	gat	gac	aaa	aga	ctg	att	880	
Val	Pro	Ser	Ala	Glu	Phe	Gln	Trp	Tyr	Lys	Asp	Asp	Lys	Arg	Leu	Ile		
			250						255						260		
gaa	gga	aag	aaa	ggg	gtg	aaa	gtg	gaa	aac	aga	cct	ttc	ctc	tca	aaa	928	
Glu	Gly	Lys	Lys	Gly	Val	Lys	Val	Glu	Asn	Arg	Pro	Phe	Leu	Ser	Lys		
			265						270						275		
ctc	atc	ttc	ttc	aat	gtc	tct	gaa	cat	gac	tat	ggg	aac	tac	act	tgc	976	
Leu	Ile	Phe	Phe	Asn	Val	Ser	Glu	His	Asp	Tyr	Gly	Asn	Tyr	Thr	Cys		
			280						285						290		
gtg	gcc	tcc	aac	aag	ctg	ggc	cac	acc	aat	gcc	agc	atc	atg	cta	ttt	1024	
Val	Ala	Ser	Asn	Lys	Leu	Gly	His	Thr	Asn	Ala	Ser	Ile	Met	Leu	Phe		
			300						305						310		
ggg	cca	ggc	gcc	gtc	agc	gag	gtg	agc	aac	ggc	acg	tgc	agg	agg	gca	1072	
Gly	Pro	Gly	Ala	Val	Ser	Glu	Val	Ser	Asn	Gly	Thr	Ser	Arg	Arg	Ala		
			315						320						325		
ggc	tgc	gtc	tgg	ctg	ccg	cct	ctt	ctg	gtc	ttg	cac	ctg	ctt	ctc	aaa	1120	
Gly	Cys	Val	Trp	Leu	Pro	Pro	Leu	Leu	Val	Leu	His	Leu	Leu	Leu	Lys		
			330						335						340		
ttt	tgat	gtg	agt	gcc	act	ccc	cac	ccg	ggg	gaa	aggg	ctgc	gcgc	cacc	accacc	1173	

His Leu Ile Val Gln Val Ser Pro Lys Ile Val Glu Ile Ser Ser Asp
130 135 140

Ile Ser Ile Asn Glu Gly Asn Asn Ile Ser Leu Thr Cys Ile Ala Thr
145 150 155 160

Gly Arg Pro Glu Pro Thr Val Thr Trp Arg His Ile Ser Pro Lys Ala
165 170 175

Val Gly Phe Val Ser Glu Asp Glu Tyr Leu Glu Ile Gln Gly Ile Thr
180 185 190

Arg Glu Gln Ser Gly Asp Tyr Glu Cys Ser Ala Ser Asn Asp Val Ala
195 200 205

Ala Pro Val Val Arg Arg Val Lys Val Thr Val Asn Tyr Pro Pro Tyr
210 215 220

Ile Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys Gly Thr
225 230 235 240

Leu Gln Cys Glu Ala Ser Ala Val Pro Ser Ala Glu Phe Gln Trp Tyr
245 250 255

Lys Asp Asp Lys Arg Leu Ile Glu Gly Lys Lys Gly Val Lys Val Glu
260 265 270

Asn Arg Pro Phe Leu Ser Lys Leu Ile Phe Phe Asn Val Ser Glu His
275 280 285

Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys Leu Gly His Thr
290 295 300

Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala Val Ser Glu Val Ser
305 310 315 320

Asn Gly Thr Ser Arg Arg Ala Gly Cys Val Trp Leu Pro Pro Leu Leu
325 330 335

Val Leu His Leu Leu Leu Lys Phe
340

<210> 5
<211> 2012
<212> DNA
<213> Homo sapiens

[illegible]

<220>

<221> CDS

<222> (501) .. (1532)

<400> 5

gccaggggaat gccaggggga aagggaattt ctgataactca gaagactcag agactgtcag 60

tttaaaaaat gaaagtaata tagaaggggc aaagtggcat ttatcattct atctctccag 120

gctcctgtct ctttaatcag ctagcctgat ttgccagta aatgattcct gagagtgtgt 180

gtgCGTgtgt gtgtgtgtgt gtgcccgcgc gcgtgtgttg tagctctgtc aatccttqqa 240

ttagaaccaa tgattgcagc ttgtaagagg gctgtccagg gccagattgt acaatgtgtc 300

tcagtgccag agtatgagtg gagataatta cggagaagtc atactctctc acaccctcgg 360

ctttcttggt gtgtccttca gcaaaacagt ggatttaa at ctccttgca aagcttgag 420

gcaacacaat ctatcaggaa agaaagaaag aaaaaaaccg aacctgacaa aaaagaagaa 480

aaagaagaag aaaaaaaatc atg aaa acc atc cag cca aaa atg cac aat tct 533

Met Lys Thr Ile Gln Pro Lys Met His Asn Ser

1

5

10

atc tct tgg gca atc ttc acg ggg ctg gct gct ctg tgt ctc ttc caa 581

Ile Ser Trp Ala Ile Phe Thr Gly Leu Ala Ala Leu Cys Leu Phe Gln

15

20

25

gga gtg ccc gtg cgc agc gga gat gcc acc ttc ccc aaa gct atg gac 629

Gly Val Pro Val Arg Ser Gly Asp Ala Thr Phe Pro Lys Ala Met Asp

30

35

40

aac gtg acg gtc cgg cag ggg gag agc gcc acc ctc agg tgc act att 677

Asn Val Thr Val Arg Gln Gly Glu Ser Ala Thr Leu Arg Cys Thr Ile

45

50

55

gac aac cgg gtc acc cgg gtg gcc tgg cta aac cgc agc acc atc ctc 725

Asp Asn Arg Val Thr Arg Val Ala Trp Leu Asn Arg Ser Thr Ile Leu

60

65

70

75

tat gct ggg aat gac aag tgg tgc ctg gat cct cgc gtg gtc ctt ctg 773

Tyr Ala Gly Asn Asp Lys Trp Cys Leu Asp Pro Arg Val Val Leu Leu

80

85

90

agc aac acc caa acg cag tac agc atc gag atc cag aac gtg gat gtg 821

Ser Asn Thr Gln Thr Gln Tyr Ser Ile Glu Ile Gln Asn Val Asp Val

95	100	105	
tat gac gag ggc cct tac acc tgc tgc gtg cag aca gac aac cac cca			869
Tyr Asp Glu Gly Pro Tyr Thr Cys Ser Val Gln Thr Asp Asn His Pro			
110	115	120	
aag acc tct agg gtc cac ctc att gtg caa gta tct ccc aaa att gta			917
Lys Thr Ser Arg Val His Leu Ile Val Gln Val Ser Pro Lys Ile Val			
125	130	135	
gag att tct tca gat atc tcc att aat gaa ggg aac aat att agc ctc			965
Glu Ile Ser Ser Asp Ile Ser Ile Asn Glu Gly Asn Asn Ile Ser Leu			
140	145	150	155
acc tgc ata gca act ggt aga cca gag cct acg gtt act tgg aga cac			1013
Thr Cys Ile Ala Thr Gly Arg Pro Glu Pro Thr Val Thr Trp Arg His			
160	165	170	
atc tct ccc aaa gcg gtt ggc ttt gtg agt gaa gac gaa tac ttg gaa			1061
Ile Ser Pro Lys Ala Val Gly Phe Val Ser Glu Asp Glu Tyr Leu Glu			
175	180	185	
att cag ggc atc acc cgg gag cag tca ggg gac tac gag tgc agt gcc			1109
Ile Gln Gly Ile Thr Arg Glu Gln Ser Gly Asp Tyr Glu Cys Ser Ala			
190	195	200	
tcc aat gac gtg gcc gcg ccc gtg gta cgg aga gta aag gtc acc gtg			1157
Ser Asn Asp Val Ala Ala Pro Val Val Arg Arg Val Lys Val Thr Val			
205	210	215	
aac tat cca cca tac att tca gaa gcc aag ggt aca ggt gtc ccc gtg			1205
Asn Tyr Pro Pro Tyr Ile Ser Glu Ala Lys Gly Thr Gly Val Pro Val			
220	225	230	235
gga caa aag ggg aca ctg cag tgt gaa gcc tca gca gtc ccc tca gca			1253
Gly Gln Lys Gly Thr Leu Gln Cys Glu Ala Ser Ala Val Pro Ser Ala			
240	245	250	
gaa ttc cag tgg tac aag gat gac aaa aga ctg att gaa gga aag aaa			1301
Glu Phe Gln Trp Tyr Lys Asp Asp Lys Arg Leu Ile Glu Gly Lys Lys			
255	260	265	
ggg gtg aaa gtg gaa aac aga cct ttc ctc tca aaa ctc atc ttc ttc			1349
Gly Val Lys Val Glu Asn Arg Pro Phe Leu Ser Lys Leu Ile Phe Phe			
270	275	280	
aat gtc tct gaa cat gac tat ggg aac tac act tgc gtg gcc tcc aac			1397
Asn Val Ser Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn			

Arg Val Ala Trp Leu Asn Arg Ser Thr Ile Leu Tyr Ala Gly Asn Asp
65 70 75 80

Lys Trp Cys Leu Asp Pro Arg Val Val Leu Leu Ser Asn Thr Gln Thr
85 90 95

Gln Tyr Ser Ile Glu Ile Gln Asn Val Asp Val Tyr Asp Glu Gly Pro
100 105 110

Tyr Thr Cys Ser Val Gln Thr Asp Asn His Pro Lys Thr Ser Arg Val
115 120 125

His Leu Ile Val Gln Val Ser Pro Lys Ile Val Glu Ile Ser Ser Asp
130 135 140

Ile Ser Ile Asn Glu Gly Asn Asn Ile Ser Leu Thr Cys Ile Ala Thr
145 150 155 160

Gly Arg Pro Glu Pro Thr Val Thr Trp Arg His Ile Ser Pro Lys Ala
165 170 175

Val Gly Phe Val Ser Glu Asp Glu Tyr Leu Glu Ile Gln Gly Ile Thr
180 185 190

Arg Glu Gln Ser Gly Asp Tyr Glu Cys Ser Ala Ser Asn Asp Val Ala
195 200 205

Ala Pro Val Val Arg Arg Val Lys Val Thr Val Asn Tyr Pro Pro Tyr
210 215 220

Ile Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys Gly Thr
225 230 235 240

Leu Gln Cys Glu Ala Ser Ala Val Pro Ser Ala Glu Phe Gln Trp Tyr
245 250 255

Lys Asp Asp Lys Arg Leu Ile Glu Gly Lys Lys Gly Val Lys Val Glu
260 265 270

Asn Arg Pro Phe Leu Ser Lys Leu Ile Phe Phe Asn Val Ser Glu His
275 280 285

Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys Leu Gly His Thr
290 295 300

Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala Val Ser Glu Val Ser
305 310 315 320

40	45	50	
agg att aag aaa ctg atc aat ggg aac ggc atg cct gtt gca gag gag			729
Arg Ile Lys Lys Leu Ile Asn Gly Asn Gly Met Pro Val Ala Glu Glu			
55	60	65	
ctt ccc tgg gaa atg tca cac aca gaa cat caa tct tcc ttc ccc act			777
Leu Pro Trp Glu Met Ser His Thr Glu His Gln Ser Ser Phe Pro Thr			
70	75	80	
cct gag atc cct cat tct ttg gca cca gga aca gtt gca att agt aaa			825
Pro Glu Ile Pro His Ser Leu Ala Pro Gly Thr Val Ala Ile Ser Lys			
85	90	95	
ccc tgg ttc cct gct gtc tca caa atc gca aga gtc caa cgt gtg gat			873
Pro Trp Phe Pro Ala Val Ser Gln Ile Ala Arg Val Gln Arg Val Asp			
100	105	110	115
ata aac ttt tgt tca tgg gag gat ctt tct ccc agt gga aaa gca act			921
Ile Asn Phe Cys Ser Trp Glu Asp Leu Ser Pro Ser Gly Lys Ala Thr			
120	125	130	
ggg aaa agc agg aca cac tgc aca gtg act gca gtt tca tcc aat gcc			969
Gly Lys Ser Arg Thr His Cys Thr Val Thr Ala Val Ser Ser Asn Ala			
135	140	145	
acc acc cat gca ggc ata aat aat gaa cat gga tgg ggg agt ctg gag			1017
Thr Thr His Ala Gly Ile Asn Asn Glu His Gly Trp Gly Ser Leu Glu			
150	155	160	
ctg ctg aat tgaggaagaa agaacacaga aattaaaatt ctcacaaagg			1066
Leu Leu Asn			
165			
ttaccattaa gctagaggaa gaccacacca ctgtgtgtcc acaaagatac agagccaggc			1126
cggtttcagc catgctgggtc atctgctcta tataatacaa ttatttagag atgggtgggta			1186
gagaacaact acagaaaaaa aaaaaaaaaa aaaaaaaaaa aa			1228

<210> 8

<211> 166

<212> PRT

<213> Homo sapiens

<400> 8

Met Asn Phe Leu Lys Leu Ile Ala Val Phe Ile Val Phe Ser His Ala

[illegible]

```
<210> 9
<211> 1917
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> (410) .. (889)
```

```
<400> 9
acgcgtcaca taaaggaaaag atacgtttta atcatcttta caagtgcgtc cttgtacctt 60
tcgggataac ctgtactgat ttctctgcag gaccttttca aagaatcctc ttcaagagag 120
aaacaaaattt taggctgacg acttcacgga gaggcagggt ctgctgttgc caatgaacga 180
```

gaacttttcta ctaggctggc ggcacgcaga gcccacgtct gtcagctgcc accttcgtaa 240

agcacacggtt tcacatgcat gagctcgagt ggctagaact tcaaaactgt gctcaggttt 300

ttgttttggga agttataaaa aagttgctca caaacaatag ttattgcctt ttatatcttt 360

tatgttagtc tactagtcag cattctgccc aaaatggaaa gccactccc atg gga agg 418

Met Gly Arg

1

gag ggg gta gca gct ggg agt ctg ctc ttc cag ctg ggg gcc ctc cca 466

Glu Gly Val Ala Ala Gly Ser Leu Leu Phe Gln Leu Gly Ala Leu Pro

5

10

15

ccc cca tgg gga gga aag acg tca agc tcc agc cac tgg ccc' cgg tgg 514

Pro Pro Trp Gly Gly Lys Thr Ser Ser Ser Ser His Trp Pro Arg Trp

20

25

30

35

gtc cca aag ccc cac ccc tca tgc tct cct ctg gtc acc tct att tac 562

Val Pro Lys Pro His Pro Ser Cys Ser Pro Leu Val Thr Ser Ile Tyr

40

45

50

gct cac atg ccc ctt cct gtc ctt cac ctg cac gtc acc agc agg tcc 610

Ala His Met Pro Leu Pro Val Leu His Leu His Val Thr Ser Arg Ser

55

60

65

cgc caa ccc caa atc tat ctg gtg aaa acc tgg aga aca aga gcg gag 658

Arg Gln Pro Gln Ile Tyr Leu Val Lys Thr Trp Arg Thr Arg Ala Glu

70

75

80

tct aag aga gat gta aat gaa aac aca gat caa cag aca cac cag aag 706

Ser Lys Arg Asp Val Asn Glu Asn Thr Asp Gln Gln Thr His Gln Lys

85

90

95

gga agc gtt gtt tcc gcg ggg aaa gga gat gga aag ggg aag aga agt 754

Gly Ser Val Val Ser Ala Gly Lys Gly Asp Gly Lys Gly Lys Arg Ser

100

105

110

115

gaa gaa ttc tgc gcc cga agc tcg ggt tgg tgt ttg ctc aac tgc ttt 802

Glu Glu Phe Cys Ala Arg Ser Ser Gly Trp Cys Leu Leu Asn Cys Phe

120

125

130

act cat ttt aac cct ttc acc tat cct ggg aga aac cca ggc ttg tca 850

Thr His Phe Asn Pro Phe Thr Tyr Pro Gly Arg Asn Pro Gly Leu Ser

135

140

145

cct ttt cat gtt ggg ttg ttt gtt tat tgg cct ctt aag tgagaattga 899

Pro Phe His Val Gly Leu Phe Val Tyr Trp Pro Leu Lys
150 155 160

tccgtgaagg gaaacagaca ggaggaggtc agattgcgaa tacctggggc ttcctagggt 959
ccagtgcggc agttaccgca cctgccttca ccggtgaacc tttagccagc tgaacaacca 1019
ccaaagcgcc ctgcagagac aagtcattca gccctctggc atgtccctgg tagcccgggc 1079
accagccgct gcggcttggt aggggcacca tgctccacc caccggggacc ttcacagttg 1139
gaaaaaagaa gaggaaaaac taattccttc ggtaacagtt tattttcatt tttgggaaag 1199
gcaaaaccac tacctggaac tcggtgcctc cgtgggttaac tttcctatct tgcttgatgat 1259
ttaaaaggctg ttctgggtca ggggggaaaa ggtgtctcct tcggtaggga atatataacg 1319
tggtgataac ctgtcactag gcagaagcat ccactctgca gggacagtgg cccctcagga 1379
aagcccgccg ctctggcca aggcctctct gcagactcca cgggggctca ccctctgccg 1439
tcaggcgact ctgaaattcc gacatttctc ccttaaagtc tcaacagaca caagagaagt 1499
ttccatcaag caagcactga catatttata ttaaaaaata gtgcaaaatc tcaacattta 1559
tataaataac tctaaacccc tgctttgtaa tttttttctt tacaaggtaa tacacacttt 1619
ctgacttggc actcaaaaat tgccattttt ttcctcttct agttcagaaa acaacttttt 1679
tttttaatag gcctcttcta atacaaaaat actcctgccc tcgcacatac agtttctctt 1739
atcttatata tatttatata tataatattg cagatcttta aacaaagggt ttgtgcaaat 1799
atgtctttta agttaagtga aattatcata aacaaaagaa aataagcatt cagcacgca 1859
gctcaactag aaacaagaaa gactactgta gaaatttttt ttcttttgcc ttcaagac 1917

<210> 10
<211> 160
<212> PRT
<213> Homo sapiens

<400> 10
Met Gly Arg Glu Gly Val Ala Ala Gly Ser Leu Leu Phe Gln Leu Gly
1 5 10 15
Ala Leu Pro Pro Pro Trp Gly Gly Lys Thr Ser Ser Ser Ser His Trp

20 25 30
 Pro Arg Trp Val Pro Lys Pro His Pro Ser Cys Ser Pro Leu Val Thr
 35 40 45
 Ser Ile Tyr Ala His Met Pro Leu Pro Val Leu His Leu His Val Thr
 50 55 60
 Ser Arg Ser Arg Gln Pro Gln Ile Tyr Leu Val Lys Thr Trp Arg Thr
 65 70 75 80
 Arg Ala Glu Ser Lys Arg Asp Val Asn Glu Asn Thr Asp Gln Gln Thr
 85 90 95
 His Gln Lys Gly Ser Val Val Ser Ala Gly Lys Gly Asp Gly Lys Gly
 100 105 110
 Lys Arg Ser Glu Glu Phe Cys Ala Arg Ser Ser Gly Trp Cys Leu Leu
 115 120 125
 Asn Cys Phe Thr His Phe Asn Pro Phe Thr Tyr Pro Gly Arg Asn Pro
 130 135 140
 Gly Leu Ser Pro Phe His Val Gly Leu Phe Val Tyr Trp Pro Leu Lys
 145 150 155 160

<210> 11
 <211> 1279
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (410)..(892)

<220>
 <221> misc_feature
 <222> (1225)..(1279)
 <223> where any n may be an a or t or g or c

<400> 11
 acgcgtcaca taaaggaaag atacgtttta atcatcttta caagtgcgtc cttgtacctt 60
 tcgggataac ctgtactgat ttctctgcag gaccttttca aagaatcctc ttcaagagag 120
 aaacaaattt taggctgacg acttcacgga gaggcaggtt ctgctgttgc caatgaacga 180

ctg	acc	ctc	cgc	gag	ttc	tac	atg	gcc	ttc	caa	gtg	gtt	cag	ctc	agc	519
Leu	Thr	Leu	Arg	Glu	Phe	Tyr	Met	Ala	Phe	Gln	Val	Val	Gln	Leu	Ser	
			95					100					105			
ctc	gcc	ccc	gag	gac	agg	gtc	agt	gtg	acc	aca	gtg	acc	gtg	ggg	ctg	567
Leu	Ala	Pro	Glu	Asp	Arg	Val	Ser	Val	Thr	Thr	Val	Thr	Val	Gly	Leu	
		110					115					120				
agc	aca	gtg	ctg	acc	tgc	gcc	gtc	cat	gga	gac	ctg	agg	cca	cca	atc	615
Ser	Thr	Val	Leu	Thr	Cys	Ala	Val	His	Gly	Asp	Leu	Arg	Pro	Pro	Ile	
		125				130					135					
atc	tgg	aag	cgc	aac	ggg	ctc	acc	ctg	aac	ttc	ctg	gac	ttg	gaa	gac	663
Ile	Trp	Lys	Arg	Asn	Gly	Leu	Thr	Leu	Asn	Phe	Leu	Asp	Leu	Glu	Asp	
140					145					150					155	
atc	aat	gac	ttt	gga	gag	gat	gat	tcc	ctg	tac	atc	acc	aag	gtg	acc	711
Ile	Asn	Asp	Phe	Gly	Glu	Asp	Asp	Ser	Leu	Tyr	Ile	Thr	Lys	Val	Thr	
			160						165					170		
acc	atc	cac	atg	ggc	aat	tac	acc	tgc	cat	gct	tcc	ggc	cac	gag	cag	759
Thr	Ile	His	Met	Gly	Asn	Tyr	Thr	Cys	His	Ala	Ser	Gly	His	Glu	Gln	
			175					180					185			
ctg	ttc	cag	acc	cac	gtc	ctg	cag	gtg	aat	gtg	ccg	cca	gtc	atc	cgt	807
Leu	Phe	Gln	Thr	His	Val	Leu	Gln	Val	Asn	Val	Pro	Pro	Val	Ile	Arg	
		190					195					200				
gtc	tat	cca	gag	agc	cag	gca	cag	gag	cct	gga	gtg	gca	gcc	agc	cta	855
Val	Tyr	Pro	Glu	Ser	Gln	Ala	Gln	Glu	Pro	Gly	Val	Ala	Ala	Ser	Leu	
	205					210					215					
aga	tgc	cat	gct	gag	ggc	att	ccc	atg	ccc	aga	atc	act	tgg	ctg	aaa	903
Arg	Cys	His	Ala	Glu	Gly	Ile	Pro	Met	Pro	Arg	Ile	Thr	Trp	Leu	Lys	
220					225				230						235	
aac	ggc	gtg	gat	gtc	tca	act	cag	atg	tcc	aaa	cag	ctc	tcc	ctt	tta	951
Asn	Gly	Val	Asp	Val	Ser	Thr	Gln	Met	Ser	Lys	Gln	Leu	Ser	Leu	Leu	
				240					245					250		
gcc	aat	ggg	agc	gaa	ctc	cac	atc	agc	agt	gtt	cgg	tat	gaa	gac	aca	999
Ala	Asn	Gly	Ser	Glu	Leu	His	Ile	Ser	Ser	Val	Arg	Tyr	Glu	Asp	Thr	
			255					260					265			
ggg	gca	tac	acc	tgc	att	gcc	aaa	aat	gaa	gtg	ggg	gtg	gat	gaa	gat	1047
Gly	Ala	Tyr	Thr	Cys	Ile	Ala	Lys	Asn	Glu	Val	Gly	Val	Asp	Glu	Asp	
		270					275					280				

Lys Gln Asp Leu Asp Glu Asp Leu Leu Gly Cys Ser Pro Gly Asp Leu
 65 70 75 80
 Leu Arg Phe Asp Asp Tyr Asn Ser Asp Ser Ser Leu Thr Leu Arg Glu
 85 90 95
 Phe Tyr Met Ala Phe Gln Val Val Gln Leu Ser Leu Ala Pro Glu Asp
 100 105 110
 Arg Val Ser Val Thr Thr Val Thr Val Gly Leu Ser Thr Val Leu Thr
 115 120 125
 Cys Ala Val His Gly Asp Leu Arg Pro Pro Ile Ile Trp Lys Arg Asn
 130 135 140
 Gly Leu Thr Leu Asn Phe Leu Asp Leu Glu Asp Ile Asn Asp Phe Gly
 145 150 155 160
 Glu Asp Asp Ser Leu Tyr Ile Thr Lys Val Thr Thr Ile His Met Gly
 165 170 175
 Asn Tyr Thr Cys His Ala Ser Gly His Glu Gln Leu Phe Gln Thr His
 180 185 190
 Val Leu Gln Val Asn Val Pro Pro Val Ile Arg Val Tyr Pro Glu Ser
 195 200 205
 Gln Ala Gln Glu Pro Gly Val Ala Ala Ser Leu Arg Cys His Ala Glu
 210 215 220
 Gly Ile Pro Met Pro Arg Ile Thr Trp Leu Lys Asn Gly Val Asp Val
 225 230 235 240
 Ser Thr Gln Met Ser Lys Gln Leu Ser Leu Leu Ala Asn Gly Ser Glu
 245 250 255
 Leu His Ile Ser Ser Val Arg Tyr Glu Asp Thr Gly Ala Tyr Thr Cys
 260 265 270
 Ile Ala Lys Asn Glu Val Gly Val Asp Glu Asp Ile Ser Ser Leu Phe
 275 280 285
 Ile Glu Asp Ser Ala Arg Lys Thr Leu Ala Asn Ile Leu Trp Arg Glu
 290 295 300
 Glu Gly Thr Lys Leu His Cys Phe Ala Ser Cys Leu
 305 310 315

gag	ccc	gaa	tgc	cag	tgc	ctg	gag	gca	tgc	agg	ccc	agc	tac	gtg	cct	704
Glu	Pro	Glu	Cys	Gln	Cys	Leu	Glu	Ala	Cys	Arg	Pro	Ser	Tyr	Val	Pro	
85						90					95					
gtg	tgc	ggc	tct	gat	ggg	agg	ttt	tat	gaa	aac	cac	tgt	aag	ctc	cac	752
Val	Cys	Gly	Ser	Asp	Gly	Arg	Phe	Tyr	Glu	Asn	His	Cys	Lys	Leu	His	
100					105					110					115	
cgt	gct	gct	tgc	ctc	ctg	gga	aag	agg	atc	acc	gtc	atc	cac	agc	aag	800
Arg	Ala	Ala	Cys	Leu	Leu	Gly	Lys	Arg	Ile	Thr	Val	Ile	His	Ser	Lys	
				120					125					130		
gac	tgt	ttc	ctc	aaa	ggg	gac	acg	tgc	acc	atg	gcc	ggc	tac	gcc	cgc	848
Asp	Cys	Phe	Leu	Lys	Gly	Asp	Thr	Cys	Thr	Met	Ala	Gly	Tyr	Ala	Arg	
			135					140					145			
ttg	aag	aat	gtc	ctt	ctg	gca	ctc	cag	acc	cgt	ctg	cag	cca	ctc	caa	896
Leu	Lys	Asn	Val	Leu	Leu	Ala	Leu	Gln	Thr	Arg	Leu	Gln	Pro	Leu	Gln	
	150						155					160				
gaa	gga	gac	agc	aga	caa	gac	cct	gcc	tcc	cag	aag	cgc	ctc	ctg	gtg	944
Glu	Gly	Asp	Ser	Arg	Gln	Asp	Pro	Ala	Ser	Gln	Lys	Arg	Leu	Leu	Val	
165						170					175					
gaa	tct	ctg	ttc	agg	gac	tta	gat	gca	gat	ggc	aat	ggc	cac	ctc	agc	992
Glu	Ser	Leu	Phe	Arg	Asp	Leu	Asp	Ala	Asp	Gly	Asn	Gly	His	Leu	Ser	
180					185					190					195	
agc	tcc	gaa	ctg	gct	cag	cat	gtg	ctg	aag	aag	cag	gac	ctg	gat	gaa	1040
Ser	Ser	Glu	Leu	Ala	Gln	His	Val	Leu	Lys	Lys	Gln	Asp	Leu	Asp	Glu	
				200					205					210		
gac	tta	ctt	ggg	tgc	tca	cca	ggg	gac	ctc	ctc	cga	ttt	gac	gat	tac	1088
Asp	Leu	Leu	Gly	Cys	Ser	Pro	Gly	Asp	Leu	Leu	Arg	Phe	Asp	Asp	Tyr	
			215					220					225			
aac	agt	gac	agc	tcc	ctg	acc	ctc	cgc	gag	ttc	tac	atg	gcc	ttc	caa	1136
Asn	Ser	Asp	Ser	Ser	Leu	Thr	Leu	Arg	Glu	Phe	Tyr	Met	Ala	Phe	Gln	
	230						235				240					
gtg	gtt	cag	ctc	agc	ctc	gcc	ccc	gag	gac	agg	gtc	agt	gtg	acc	aca	1184
Val	Val	Gln	Leu	Ser	Leu	Ala	Pro	Glu	Asp	Arg	Val	Ser	Val	Thr	Thr	
245						250					255					
gtg	acc	gtg	ggg	ctg	agc	aca	gtg	ctg	acc	tgc	gcc	gtc	cat	gga	gac	1232
Val	Thr	Val	Gly	Leu	Ser	Thr	Val	Leu	Thr	Cys	Ala	Val	His	Gly	Asp	
260					265					270					275	

—

aac atg ttc tat gtc ttc tcc gac gac ggt atc atc gtc atc cat cct 1808
Asn Met Phe Tyr Val Phe Ser Asp Asp Gly Ile Ile Val Ile His Pro
455 460 465

gtg	gac	tgt	gag	atc	cag	agg	cac	ctc	aaa	ccc	acg	gaa	aag	att	ttc	1856
Val	Asp	Cys	Glu	Ile	Gln	Arg	His	Leu	Lys	Pro	Thr	Glu	Lys	Ile	Phe	
		470					475					480				
atg	agc	tat	gaa	gaa	atc	tgt	cct	caa	aga	gaa	aaa	aat	gca	acc	cag	1904
Met	Ser	Tyr	Glu	Glu	Ile	Cys	Pro	Gln	Arg	Glu	Lys	Asn	Ala	Thr	Gln	
		485				490						495				
ccc	tgc	cag	tgg	gta	tct	gca	gtc	aat	gtc	cgg	aac	cgg	tac	atc	tat	1952
Pro	Cys	Gln	Trp	Val	Ser	Ala	Val	Asn	Val	Arg	Asn	Arg	Tyr	Ile	Tyr	
500					505					510					515	
gtg	gcc	cag	cca	gca	ctg	agc	aga	gtc	ctt	gtg	gtc	gac	atc	caa	gcc	2000
Val	Ala	Gln	Pro	Ala	Leu	Ser	Arg	Val	Leu	Val	Val	Asp	Ile	Gln	Ala	
				520					525					530		
cag	aaa	gtc	cta	cag	tcc	ata	ggc	gtg	gac	cct	ctg	ccg	gct	aag	ctg	2048
Gln	Lys	Val	Leu	Gln	Ser	Ile	Gly	Val	Asp	Pro	Leu	Pro	Ala	Lys	Leu	
		535						540					545			
tcc	tat	gac	aag	tca	cat	gac	caa	gtg	tgg	gtc	ctg	agc	tgg	ggg	gac	2096
Ser	Tyr	Asp	Lys	Ser	His	Asp	Gln	Val	Trp	Val	Leu	Ser	Trp	Gly	Asp	
		550					555					560				
gtg	cac	aag	tcc	cga	cca	agt	ctc	cag	gtg	atc	aca	gaa	gcc	agc	acc	2144
Val	His	Lys	Ser	Arg	Pro	Ser	Leu	Gln	Val	Ile	Thr	Glu	Ala	Ser	Thr	
		565				570					575					
ggc	cag	agc	cag	cac	ctc	atc	cgc	aca	ccc	ttt	gca	gga	gtg	gat	gat	2192
Gly	Gln	Ser	Gln	His	Leu	Ile	Arg	Thr	Pro	Phe	Ala	Gly	Val	Asp	Asp	
580					585					590					595	
ttc	ttc	att	ccc	cca	aca	aac	ctc	atc	atc	aac	cac	atc	agg	ttt	ggc	2240
Phe	Phe	Ile	Pro	Pro	Thr	Asn	Leu	Ile	Ile	Asn	His	Ile	Arg	Phe	Gly	
				600					605					610		
ttc	atc	ttc	aac	aag	tct	gat	cct	gca	gtc	cac	aag	gtg	gac	ctg	gaa	2288
Phe	Ile	Phe	Asn	Lys	Ser	Asp	Pro	Ala	Val	His	Lys	Val	Asp	Leu	Glu	
			615					620					625			
aca	atg	atg	ccc	ctc	aag	acc	atc	ggc	ctg	cac	cac	cat	ggc	tgc	gtg	2336
Thr	Met	Met	Pro	Leu	Lys	Thr	Ile	Gly	Leu	His	His	His	Gly	Cys	Val	
		630					635					640				
ccc	cag	gcc	atg	gca	cac	acc	cac	ctg	ggc	ggc	tac	ttc	ttc	atc	cag	2384
Pro	Gln	Ala	Met	Ala	His	Thr	His	Leu	Gly	Gly	Tyr	Phe	Phe	Ile	Gln	
		645				650					655					

tgc	cga	cag	gac	agc	ccc	gcc	tct	gct	gcc	cga	cag	ctg	ctc	gtt	gac	2432
Cys	Arg	Gln	Asp	Ser	Pro	Ala	Ser	Ala	Ala	Arg	Gln	Leu	Leu	Val	Asp	
660					665					670					675	

```

agt gtc aca gac tct gtg ctt ggc ccc aat ggt gat gta aca ggc acc      2480
Ser Val Thr Asp Ser Val Leu Gly Pro Asn Gly Asp Val Thr Gly Thr
          680                      685                      690

```

cca cac aca tcc ccc gac ggg cgc ttc ata gtc agt gct gca gct gac 2528
Pro His Thr Ser Pro Asp Gly Arg Phe Ile Val Ser Ala Ala Ala Asp
695 700 705

agc ccc tgg ctg cac gtg cag gag atc aca gtg cgg ggc gag atc cag 2576
 Ser Pro Trp Leu His Val Gln Glu Ile Thr Val Arg Gly Glu Ile Gln
 710 715 720

acc ctg tat gac ctg caa ata aac tcg ggc atc tca gac ttg gcc ttc 2624
Thr Leu Tyr Asp Leu Gln Ile Asn Ser Gly Ile Ser Asp Leu Ala Phe
725 730 735

cag cgc tcc ttc act gaa agc aat caa tac aac atc tac gcg gct ctg 2672
Gln Arg Ser Phe Thr Glu Ser Asn Gln Tyr Asn Ile Tyr Ala Ala Leu
740 745 750 755

cac acg gag ccg gac ctg ctg ttc ctg gag ctg tcc acg ggg aag gtg 2720
His Thr Glu Pro Asp Leu Leu Phe Leu Glu Leu Ser Thr Gly Lys Val
760 765 770

ggc atg ctg aag aac tta aag gag cca ccc gca ggg cca gct cag ccc 2768
Gly Met Leu Lys Asn Leu Lys Glu Pro Pro Ala Gly Pro Ala Gln Pro
775 780 785

tgg ggg ggt acc cac aga atc atg agg gac agt ggg ctg ttt gga cag 2816
 Trp Gly Gly Thr His Arg Ile Met Arg Asp Ser Gly Leu Phe Gly Gln
 790 795 800

tac ctc ctc aca cca gcc cga gag tca ctg ttc ctc atc aat ggg aga 2864
Tyr Leu Leu Thr Pro Ala Arg Glu Ser Leu Phe Leu Ile Asn Gly Arg
 805 810 815

caa aac acg ctg cgg tgt gag gtg tca ggt ata aag ggg ggg acc aca 2912
Gln Asn Thr Leu Arg Cys Glu Val Ser Gly Ile Lys Gly Gly Thr Thr
820 825 830 835

gtg gtg tgg gtg ggt gag gta tgaagggccc agagcagagc cctgggccaa 2963
Val Val Trp Val Gly Glu Val
840

ggaacacccc ctagtcctga cactgcagcc tcaagcaggt acgctgtaca tttttacaga 3023
 caaaagcaaa aacctgtact cgctttgtgg ttcaacactg gtctccttgc aagtttecta 3083
 gtataaggta tgcgctgcta ccaagattgg gggttttttcg ttaggaagta tgatttatgc 3143
 cttgagctac gatgagaaca tatgctgctg tgtaaaggga tcatttctgt gccaaagctgc 3203
 acaccgagtg acctggggac atcatggaac caagggatcc tgctctccaa gcagacacct 3263
 ctgtcagttg ccttcacata gtcattgtcc cttactgcc aacccagcca gactttgccc 3323
 tgacggagtg gcccggaagc agaggccgac caggagcagg ggcctccctc ccgaactgaa 3383
 agcccatccg tcctcgctg ggaccgcac ttctccctcg cagctgcttc ttgcttttct 3443
 ttccatttga cttgctgtaa gcctgagggg gagccaacaa gacttactgc atcttggggg 3503
 atggggaaat cactcacttt attttgaaa tttttgatta aaaaaaatt ttataatctc 3563
 aaatgctagt aagcagaaag atgctctccg aggtccaact atatccttc ctgccttagg 3623
 ccgagtctcg ggggtggtca caaccacaca tcccacagcc agaaagaaca atgggtcatct 3683
 gagaatactg gccctgtcga ctattgccac cctgcttctc caagagcaga ccaggccacc 3743
 tcatccgtaa ggactcggtt ctgtgttggg acccaaaaa accagaacaa gttctgtgtg 3803
 cctcctttca gcacagaagg gagacatctc attagtcagg tctggtacc cagattcagg 3863
 gcagactggg cttgcctggc aaggtatggg tggcctccag gctcaatgca gaaaccccaa 3923
 ggacacgagt ggggccaggt gagttcctga agctatacct tttcaaaaca gattttgttt 3983
 tcctacctgt ggcccatcca ctctctctg gtaccccatc cccgcatcag cactgcagag 4043
 agaacacatt tcggcgaggg ttttcttacc cacattcccc aatcaatata cacacactgc 4103
 agaaccaga acagaaggcc acaggtggc actactgcat tctccttatg tgtctcaggc 4163
 tgtggtgact ctcacatggg catcgaagaa gtacaacca catagccctc tggagaccgc 4223
 ctagatcaga gactcagcaa aaacaggtc gccttcctc tcccacatat gagtggaaact 4283
 tacatgtgtc ctggtttgaa tgatcathtt gcaagccaca cgggttgga gaggtggtct 4343
 caccacagac gtctttgcta atttgccac cttcacctac tgacatgacc aggattttcc 4403

1 5 10 15
 Leu Pro Ala Ala Leu Gly Trp Met Asp Pro Gly Thr Ser Arg Gly Pro
 20 25 30
 Asp Val Gly Val Gly Glu Ser Gln Ala Glu Glu Pro Arg Ser Phe Glu
 35 40 45
 Val Thr Arg Arg Glu Gly Leu Ser Ser His Asn Glu Leu Leu Ala Ser
 50 55 60
 Cys Gly Lys Lys Phe Cys Ser Arg Gly Ser Arg Cys Val Leu Ser Arg
 65 70 75 80
 Lys Thr Gly Glu Pro Glu Cys Gln Cys Leu Glu Ala Cys Arg Pro Ser
 85 90 95
 Tyr Val Pro Val Cys Gly Ser Asp Gly Arg Phe Tyr Glu Asn His Cys
 100 105 110
 Lys Leu His Arg Ala Ala Cys Leu Leu Gly Lys Arg Ile Thr Val Ile
 115 120 125
 His Ser Lys Asp Cys Phe Leu Lys Gly Asp Thr Cys Thr Met Ala Gly
 130 135 140
 Tyr Ala Arg Leu Lys Asn Val Leu Leu Ala Leu Gln Thr Arg Leu Gln
 145 150 155 160
 Pro Leu Gln Glu Gly Asp Ser Arg Gln Asp Pro Ala Ser Gln Lys Arg
 165 170 175
 Leu Leu Val Glu Ser Leu Phe Arg Asp Leu Asp Ala Asp Gly Asn Gly
 180 185 190
 His Leu Ser Ser Ser Glu Leu Ala Gln His Val Leu Lys Lys Gln Asp
 195 200 205
 Leu Asp Glu Asp Leu Leu Gly Cys Ser Pro Gly Asp Leu Leu Arg Phe
 210 215 220
 Asp Asp Tyr Asn Ser Asp Ser Ser Leu Thr Leu Arg Glu Phe Tyr Met
 225 230 235 240
 Ala Phe Gln Val Val Gln Leu Ser Leu Ala Pro Glu Asp Arg Val Ser
 245 250 255
 Val Thr Thr Val Thr Val Gly Leu Ser Thr Val Leu Thr Cys Ala Val

[illegible][illegible]

770

775

780

Ala Gln Pro Trp Gly Gly Thr His Arg Ile Met Arg Asp Ser Gly Leu
785 790 795 800

Phe Gly Gln Tyr Leu Leu Thr Pro Ala Arg Glu Ser Leu Phe Leu Ile
805 810 815

Asn Gly Arg Gln Asn Thr Leu Arg Cys Glu Val Ser Gly Ile Lys Gly
820 825 830

Gly Thr Thr Val Val Trp Val Gly Glu Val
835 840

<210> 17

<211> 5502

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (420) .. (2864)

<400> 17

caatttcaca caggaaacag ctatgccatg attacgcaag ttggtaccga gctcggatcc 60

actagtaacg gccgccagtg tgctggaatt cggcttactc actatagggc tcgagcggct 120

gcccgggcag gtcattaatt ccatttcctt ttagagtatc acagctttct ccttcactga 180

ccaccctttg cttcctgtca gaaagccctg gacagaactc tctgtgggat tctgcccag 240

tttctgagat atcgctcaa ttgtcctggc tgggctgtcg ggtctgcccg ttttacagat 300

gggcaaaactg gagtgggaag tatccgggtg gcttcctcag gcctgcagct ggtggagcag 360

ctactgaaac aatcaggagc ccagaagctt tgaagtcaca agaagagaag actcccaga 419

atg cag tgt gat gtt ggt gat gga cgc ctg ttt cgc ctt tca ctt aaa 467

Met Gln Cys Asp Val Gly Asp Gly Arg Leu Phe Arg Leu Ser Leu Lys

1

5

10

15

cgt gcc ctt tcc agc tgc cct gac ctc ttt ggg ctt tcc agc cgc aac 515

Arg Ala Leu Ser Ser Cys Pro Asp Leu Phe Gly Leu Ser Ser Arg Asn

20

25

30

gag ctg ctg gcc tcc tgc ggg aag aag ttc tgc agc cga ggg agc cgg 563

Glu Leu Leu Ala Ser Cys Gly Lys Lys Phe Cys Ser Arg Gly Ser Arg
35 40 45

tgc gtg ctc agc agg aag aca ggg gag ccc gaa tgc cag tgc ctg gag 611
Cys Val Leu Ser Arg Lys Thr Gly Glu Pro Glu Cys Gln Cys Leu Glu
50 55 60

gca tgc agg ccc agc tac gtg cct gtg tgc ggc tct gat ggg agg ttt 659
Ala Cys Arg Pro Ser Tyr Val Pro Val Cys Gly Ser Asp Gly Arg Phe
65 70 75 80

tat gaa aac cac tgt aag ctc cac cgt gct gct tgc ctc ctg gga aag 707
Tyr Glu Asn His Cys Lys Leu His Arg Ala Ala Cys Leu Leu Gly Lys
85 90 95

agg atc acc gtc atc cac agc aag gac tgt ttc ctc aaa ggt gac acg 755
Arg Ile Thr Val Ile His Ser Lys Asp Cys Phe Leu Lys Gly Asp Thr
100 105 110

tgc acc atg gcc ggc tac gcc cgc ttg aag aat gtc ctt ctg gca ctc 803
Cys Thr Met Ala Gly Tyr Ala Arg Leu Lys Asn Val Leu Leu Ala Leu
115 120 125

cag acc cgt ctg cag cca ctc caa gaa gga gac agc aga caa gac cct 851
Gln Thr Arg Leu Gln Pro Leu Gln Glu Gly Asp Ser Arg Gln Asp Pro
130 135 140

gcc tcc cag aag cgc ctc ctg gtg gaa tct ctg ttc agg gac tta gat 899
Ala Ser Gln Lys Arg Leu Leu Val Glu Ser Leu Phe Arg Asp Leu Asp
145 150 155 160

gca gat ggc aat ggc cac ctc agc agc tcc gaa ctg gct cag cat gtg 947
Ala Asp Gly Asn Gly His Leu Ser Ser Ser Glu Leu Ala Gln His Val
165 170 175

ctg aag aag cag gac ctg gat gaa gac tta ctt ggt tgc tca cca ggt 995
Leu Lys Lys Gln Asp Leu Asp Glu Asp Leu Leu Gly Cys Ser Pro Gly
180 185 190

gac ctc ctc cga ttt gac gat tac aac agt gac agc tcc ctg acc ctc 1043
Asp Leu Leu Arg Phe Asp Asp Tyr Asn Ser Asp Ser Ser Leu Thr Leu
195 200 205

cgc gag ttc tac atg gcc ttc caa gtg gtt cag ctc agc ctc gcc ccc 1091
Arg Glu Phe Tyr Met Ala Phe Gln Val Val Gln Leu Ser Leu Ala Pro
210 215 220

gag gac agg gtc agt gtg acc aca gtg acc gtg ggg ctg agc aca gtg 1139

6-10-78

$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{x}} \right) = \frac{\partial L}{\partial x}$

Gly Leu His His His Gly Cys Val Pro Gln Ala Met Ala His Thr His	
610 615 620	
ctg ggc ggc tac ttc ttc atc cag tgc cga cag gac agc ccc gcc tct	2339
Leu Gly Gly Tyr Phe Phe Ile Gln Cys Arg Gln Asp Ser Pro Ala Ser	
625 630 635 640	
gct gcc cga cag ctg ctc gtt gac agt gtc aca gac tct gtg ctt ggc	2387
Ala Ala Arg Gln Leu Leu Val Asp Ser Val Thr Asp Ser Val Leu Gly	
645 650 655	
ccc aat ggt gat gta aca ggc acc cca cac aca tcc ccc gac ggg cgc	2435
Pro Asn Gly Asp Val Thr Gly Thr Pro His Thr Ser Pro Asp Gly Arg	
660 665 670	
ttc ata gtc agt gct gca gct gac agc ccc tgg ctg cac gtg cag gag	2483
Phe Ile Val Ser Ala Ala Ala Asp Ser Pro Trp Leu His Val Gln Glu	
675 680 685	
atc aca gtg cgg ggc gag atc cag acc ctg tat gac ctg caa ata aac	2531
Ile Thr Val Arg Gly Glu Ile Gln Thr Leu Tyr Asp Leu Gln Ile Asn	
690 695 700	
tgc ggc atc tca gac ttg gcc ttc cag cgc tcc ttc act gaa agc aat	2579
Ser Gly Ile Ser Asp Leu Ala Phe Gln Arg Ser Phe Thr Glu Ser Asn	
705 710 715 720	
caa tac aac atc tac gcg gct ctg cac acg gag ccg gac ctg ctg ttc	2627
Gln Tyr Asn Ile Tyr Ala Ala Leu His Thr Glu Pro Asp Leu Leu Phe	
725 730 735	
ctg gag ctg tcc acg ggg aag gtg ggc atg ctg aag aac tta aag gag	2675
Leu Glu Leu Ser Thr Gly Lys Val Gly Met Leu Lys Asn Leu Lys Glu	
740 745 750	
cca ccc gca ggg cca gct cag ccc tgg ggg ggt acc cac aga atc atg	2723
Pro Pro Ala Gly Pro Ala Gln Pro Trp Gly Gly Thr His Arg Ile Met	
755 760 765	
agg gac agt ggg ctg ttt gga cag tac ctc ctc aca cca gcc cga gag	2771
Arg Asp Ser Gly Leu Phe Gly Gln Tyr Leu Leu Thr Pro Ala Arg Glu	
770 775 780	
tca ctg ttc ctc atc aat ggg aga caa aac acg ctg cgg tgt gag gtg	2819
Ser Leu Phe Leu Ile Asn Gly Arg Gln Asn Thr Leu Arg Cys Glu Val	
785 790 795 800	
tca ggt ata aag ggg ggg acc aca gtg gtg tgg gtg ggt gag gta	2864

Ser Gly Ile Lys Gly Gly Thr Thr Val Val Trp Val Gly Glu Val
805 810 815

39

gcaagccaca cgggttgga gaggtggtct caccacagac gtctttgcta atttgccac 4304
cttcacctac tgacatgacc aggattttcc ttgcccatta aggaatgaac tctttcaagg 4364
agaggaaacc ctagactctg tgtcactctc aacacacaca gtcctttca ctctgcctg 4424
actgccaagc caactgcac ccccgcccca gatctcatga gatcaatcac ttgtatgtct 4484
cacgcaactt ggtccaccaa acgctgtcc cctgtaactc ctaggggtgc gcctagacag 4544
gtacgtctgt tttttatattt aaaagatatg ctatgtagat ataagttgag gaagctcacc 4604
tcaaagcct agaatgcagt ttcacagtag ctgggatgca tggatgacct atctacccc 4664
tttttttttc ctgctcaat atcttgatat gttatgttta ctcccaatct cccattttta 4724
ccactaaaat tctccaactt tcataaactt ttttttgaa aaatttccat tgtatcagcc 4784
cctgacagaa aaaggatctc tgagcctaaa ggaggaaaag tcccaccaac taccagacca 4844
gaacacgagc cctctgggc agcaggattc ctaagtcaaa gaccagtttg acccaaactg 4904
gccttttaaa ataatcagga gtgacagagt caacttctgc agcacctgct tctccccac 4964
tgtcccttc atcttggaat gtgtctaaaa aagcatagct gccctttgct gtcctcagag 5024
tgcatttctt ggagacggca ggcttaggtc tcaactgacag catgccagac acaactgaat 5084
cgaagcaggc ctgaagccta ggtcaggggt tcaggagtcc agccccagga ggcaaagtca 5144
ccaatgcagg gaggtaaatg ccttttgga ggaaaacaa tagagttggt tgggtgggga 5204
gtcaggggtg ggaggagaag gaggaagagg aggaaggcca gactggcctg ccctttctcc 5264
catacttcac cccagcagag gttcatggga cacagttgga aagccactgg gaggaaatgc 5324
ctcactacag gggggcctcc ttagcaagc ccagccggtc atcctcctaa tgaaccacaca 5384
aggtaattc acaactgata tcttagctat taaagaagta ctgactttac caaaagaatc 5444
atcaagaaag ctatttatat aaacccctc agtcattttg aaataaaaatt aattttac 5502

<210> 18

<211> 815

<212> PRT

<213> Homo sapiens

<400> 18

Met Gln Cys Asp Val Gly Asp Gly Arg Leu Phe Arg Leu Ser Leu Lys
1 5 10 15

Arg Ala Leu Ser Ser Cys Pro Asp Leu Phe Gly Leu Ser Ser Arg Asn
20 25 30

Glu Leu Leu Ala Ser Cys Gly Lys Lys Phe Cys Ser Arg Gly Ser Arg
35 40 45

Cys Val Leu Ser Arg Lys Thr Gly Glu Pro Glu Cys Gln Cys Leu Glu
50 55 60

Ala Cys Arg Pro Ser Tyr Val Pro Val Cys Gly Ser Asp Gly Arg Phe
65 70 75 80

Tyr Glu Asn His Cys Lys Leu His Arg Ala Ala Cys Leu Leu Gly Lys
85 90 95

Arg Ile Thr Val Ile His Ser Lys Asp Cys Phe Leu Lys Gly Asp Thr
100 105 110

Cys Thr Met Ala Gly Tyr Ala Arg Leu Lys Asn Val Leu Leu Ala Leu
115 120 125

Gln Thr Arg Leu Gln Pro Leu Gln Glu Gly Asp Ser Arg Gln Asp Pro
130 135 140

Ala Ser Gln Lys Arg Leu Leu Val Glu Ser Leu Phe Arg Asp Leu Asp
145 150 155 160

Ala Asp Gly Asn Gly His Leu Ser Ser Ser Glu Leu Ala Gln His Val
165 170 175

Leu Lys Lys Gln Asp Leu Asp Glu Asp Leu Leu Gly Cys Ser Pro Gly
180 185 190

Asp Leu Leu Arg Phe Asp Asp Tyr Asn Ser Asp Ser Ser Leu Thr Leu
195 200 205

Arg Glu Phe Tyr Met Ala Phe Gln Val Val Gln Leu Ser Leu Ala Pro
210 215 220

Glu Asp Arg Val Ser Val Thr Thr Val Thr Val Gly Leu Ser Thr Val
225 230 235 240

Leu Thr Cys Ala Val His Gly Asp Leu Arg Pro Pro Ile Ile Trp Lys

245	250	255
Arg Asn Gly Leu Thr Leu Asn Phe Leu Asp Leu Glu Asp Ile Asn Asp		
260	265	270
Phe Gly Glu Asp Asp Ser Leu Tyr Ile Thr Lys Val Thr Thr Ile His		
275	280	285
Met Gly Asn Tyr Thr Cys His Ala Ser Gly His Glu Gln Leu Phe Gln		
290	295	300
Thr His Val Leu Gln Val Asn Val Pro Pro Val Ile Arg Val Tyr Pro		
305	310	315
Glu Ser Gln Ala Gln Glu Pro Gly Val Ala Ala Ser Leu Arg Cys His		
325	330	335
Ala Glu Gly Ile Pro Met Pro Arg Ile Thr Trp Leu Lys Asn Gly Val		
340	345	350
Asp Val Ser Thr Gln Met Ser Lys Gln Leu Ser Leu Leu Ala Asn Gly		
355	360	365
Ser Glu Leu His Ile Ser Ser Val Arg Tyr Glu Asp Thr Gly Ala Tyr		
370	375	380
Thr Cys Ile Ala Lys Asn Glu Val Gly Val Asp Glu Asp Ile Ser Ser		
385	390	395
Leu Phe Ile Glu Asp Ser Ala Arg Lys Thr Leu Ala Asn Ile Leu Trp		
405	410	415
Arg Glu Glu Gly Leu Ser Val Gly Asn Met Phe Tyr Val Phe Ser Asp		
420	425	430
Asp Gly Ile Ile Val Ile His Pro Val Asp Cys Glu Ile Gln Arg His		
435	440	445
Leu Lys Pro Thr Glu Lys Ile Phe Met Ser Tyr Glu Glu Ile Cys Pro		
450	455	460
Gln Arg Glu Lys Asn Ala Thr Gln Pro Cys Gln Trp Val Ser Ala Val		
465	470	475
Asn Val Arg Asn Arg Tyr Ile Tyr Val Ala Gln Pro Ala Leu Ser Arg		
485	490	495
Val Leu Val Val Asp Ile Gln Ala Gln Lys Val Leu Gln Ser Ile Gly		

[illegible]

1990-1991

755					760					765					
Arg	Asp	Ser	Gly	Leu	Phe	Gly	Gln	Tyr	Leu	Leu	Thr	Pro	Ala	Arg	Glu
770					775					780					
Ser	Leu	Phe	Leu	Ile	Asn	Gly	Arg	Gln	Asn	Thr	Leu	Arg	Cys	Glu	Val
785					790					795					800
Ser	Gly	Ile	Lys	Gly	Gly	Thr	Thr	Val	Val	Trp	Val	Gly	Glu	Val	
805					810					815					

```
<210> 19
<211> 1208
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> (124) .. (1089)
```

```

<400> 19
ctttgcttca gccgcagtcg ccactggctg cctgaggtgc tcttacagcc tgttccaagt 60
gtggcttaat ccgtctccac caccagatct ttctcgtgg attcctctgc taagaccgct 120
gcc atg cca gtg acg gta acc cgc acc acc atc aca acc acc acg acg 168
Met Pro Val Thr Val Thr Arg Thr Thr Ile Thr Thr Thr Thr Thr
1 5 10 15
tca tct tcg ggc ctg ggg tcc ccc atg atc gtg ggg tcc cct cgg gcc 216
Ser Ser Ser Gly Leu Gly Ser Pro Met Ile Val Gly Ser Pro Arg Ala
20 25 30
ctg aca cag ccc ctg ggt ctc ctt cgc ctg ctg cag ctg gtg tct acc 264
Leu Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln Leu Val Ser Thr
35 40 45
tgc gtg gcc ttc tcg ctg gtg gct agc gtg ggc gcc tgg acg ggg tcc 312
Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp Thr Gly Ser
50 55 60
atg ggc aac tgg tcc atg ttc acc tgg tgc ttc tgc ttc tcc gtg acc 360
Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys Phe Ser Val Thr
65 70 75
ctg atc atc ctc atc gtg gag ctg tgc ggg ctc cag gcc cgc ttc ccc 408
Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu Gln Ala Arg Phe Pro

```

80	85	90	95	
ctg tct tgg cgc aac ttc ccc atc acc ttc gcc tgc tat gcg gcc ctc				456
Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe Ala Cys Tyr Ala Ala Leu				
	100	105	110	
ttc tgc ctc tcg gcc tcc atc atc tac ccc acc acc tat gtc cag ttc				504
Phe Cys Leu Ser Ala Ser Ile Ile Tyr Pro Thr Thr Tyr Val Gln Phe				
	115	120	125	
ctg tcc cac ggc cgt tcg cgg gac cac gcc atc gcc gcc acc ttc ttc				552
Leu Ser His Gly Arg Ser Arg Asp His Ala Ile Ala Ala Thr Phe Phe				
	130	135	140	
tcc tgc atc gcg tgt gtg gct tac gcc acc gaa gtg gcc tgg acc cgg				600
Ser Cys Ile Ala Cys Val Ala Tyr Ala Thr Glu Val Ala Trp Thr Arg				
	145	150	155	
gcc cgg ccc ggc gag atc act ggc tat atg gcc acc gta ccc ggg ctg				648
Ala Arg Pro Gly Glu Ile Thr Gly Tyr Met Ala Thr Val Pro Gly Leu				
160	165	170	175	
ctg aag gtg ctg gag acc ttc gtt gcc tgc atc atc ttc gcg ttc atc				696
Leu Lys Val Leu Glu Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile				
	180	185	190	
agc gac ccc aac ctg tac cag cac cag ccg gcc ctg gag tgg tgc gtg				744
Ser Asp Pro Asn Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val				
	195	200	205	
gcg gtg tac gcc atc tgc ttc atc cta gcg gcc atc gcc atc ctg ctg				792
Ala Val Tyr Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu				
	210	215	220	
aac ctg ggg gag tgc acc aac gtg cta ccc atc ccc ttc ccc agc ttc				840
Asn Leu Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe				
	225	230	235	
ctg tcg ggg ctg gcc ttg ctg tct gtc ctc ctc tat gcc acc gcc ctt				888
Leu Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu				
240	245	250	255	
gtt ctc tgg ccc ctc tac cag ttc gat gag aag tat ggc ggc cag cct				936
Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln Pro				
	260	265	270	
cgg cgc tcg aga gat gta agc tgc agc cgc agc cat gcc tac tac gtg				984
Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr Tyr Val				

[illegible]

cag gtc tgg cta agg tac cag aag cca aca agt ccc aga aag gtc aag 769
Gln Val Trp Leu Arg Tyr Gln Lys Pro Thr Ser Pro Arg Lys Val Lys
80 85 90

tgactttccc aaggtcacac agcaagttga tggcagagct ggggtacagga ctcaga 825

```
<210> 24
<211> 92
<212> PRT
<213> Homo sapiens
```

<400> 24
Met Asp Ile Lys Ala Val Ser Pro Ser Ser Pro Ala Thr Thr Asp Ser
1 5 10 15

Thr Ala Gly Thr Val Leu Leu Cys Phe Phe Lys Ala Trp Val Leu Gln
20 25 30

Lys Gln Leu Leu Ser Cys Thr Pro Lys Val Glu Trp Lys Ser Leu Gly

Lys Gly Gly Gly Glu Ser Val Lys Gly Met Ala Arg Arg Gly Gly Arg
50 55 60

Gln Gly Thr Gly Val Leu Ala Thr Ala Asp Gly Lys Gln Val Trp Leu
65 70 75 80

Arg Tyr Gln Lys Pro Thr Ser Pro Arg Lys Val Lys
85 90

```
<210> 25
<211> 1099
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> (83) .. (889)
```

<400> 25
ctagaattca qcqgccgctg aattctagtg cagagtqagc aagggccgcc tcattcagct 60

tctctctgag agccagggcc ac atg gct cac ctg gtg aac tcc gtc agc gac	112
Met Ala His Leu Val Asn Ser Val Ser Asp	
1 5 10	
atc ctg gat gcc ctg cag agg gac cgg ggg ctg ggc cgg ccc cgc aac	160
Ile Leu Asp Ala Leu Gln Arg Asp Arg Gly Leu Gly Arg Pro Arg Asn	
15 20 25	
aag gcc gac ctt cag aga gcg cct gcc cgg gga acc cgg ccc cgg ggc	208
Lys Ala Asp Leu Gln Arg Ala Pro Ala Arg Gly Thr Arg Pro Arg Gly	
30 35 40	
tgt gcc act ggc tcc cgg ccc cga gac tgt ctg gac gtc ctc cta agc	256
Cys Ala Thr Gly Ser Arg Pro Arg Asp Cys Leu Asp Val Leu Leu Ser	
45 50 55	
gga cag cag gac gat ggc gtc tac tct gtc ttt ccc acc cac tac ccg	304
Gly Gln Gln Asp Asp Gly Val Tyr Ser Val Phe Pro Thr His Tyr Pro	
60 65 70	
gcc ggc ttc cag gtg tac tgt gac atg cgc acg gac ggc ggc ggc tgg	352
Ala Gly Phe Gln Val Tyr Cys Asp Met Arg Thr Asp Gly Gly Gly Trp	
75 80 85 90	
acg gtg ttt cag cgc cgg gag gac ggc tcc gtg aac ttc ttc cgg ggc	400
Thr Val Phe Gln Arg Arg Glu Asp Gly Ser Val Asn Phe Phe Arg Gly	
95 100 105	
tgg gat gcg tac cga gac ggc ttt ggc agg ctc acc ggg gag cac tgg	448
Trp Asp Ala Tyr Arg Asp Gly Phe Gly Arg Leu Thr Gly Glu His Trp	
110 115 120	
cta ggg ctc aag agg atc cac gcc ctg acc aca cag gct gcc tac gag	496
Leu Gly Leu Lys Arg Ile His Ala Leu Thr Thr Gln Ala Ala Tyr Glu	
125 130 135	
ctg cac gtg gac ctg gag gac ttt gag aat ggc acg gcc tat gcc cgc	544
Leu His Val Asp Leu Glu Asp Phe Glu Asn Gly Thr Ala Tyr Ala Arg	
140 145 150	
tac ggg agc ttc ggc gtg ggc ttg ttc tcc gtg gac cct gag gaa gac	592
Tyr Gly Ser Phe Gly Val Gly Leu Phe Ser Val Asp Pro Glu Glu Asp	
155 160 165 170	
ggg tac ccg ctc acc gtg gct gac tat tcc ggc act gca ggc gac tcc	640
Gly Tyr Pro Leu Thr Val Ala Asp Tyr Ser Gly Thr Ala Gly Asp Ser	
175 180 185	

ctc ctg aag cac agc ggc atg agg ttc acc acc aag gac cgt gac agc 688
Leu Leu Lys His Ser Gly Met Arg Phe Thr Thr Lys Asp Arg Asp Ser
190 195 200

gac cat tca gag aac aac tgt gcc gcc ttc tac cgc ggt gcc tgg tgg 736
Asp His Ser Glu Asn Asn Cys Ala Ala Phe Tyr Arg Gly Ala Trp Trp
205 210 215

tac cgc aac tgc cac acg tcc aac ctc aat ggg cag tac ctg cgc ggt 784
Tyr Arg Asn Cys His Thr Ser Asn Leu Asn Gly Gln Tyr Leu Arg Gly
220 225 230

gcg cac gcc tcc tat gcc gac ggc gtg gag tgg tcc tcc tgg acc ggc 832
Ala His Ala Ser Tyr Ala Asp Gly Val Glu Trp Ser Ser Trp Thr Gly
235 240 245 250

tgg cag tac tca ctc aag ttc tct gag atg aag atc cgg ccg gtc cgg 880
 Trp Gln Tyr Ser Leu Lys Phe Ser Glu Met Lys Ile Arg Pro Val Arg
 255 260 265

gag gac cgc tagaccggtg caccttgtcc ttggccctgc tggtcctgt 929
Glu Asp Arg

cqccccatcc ccgacccccac ctcactcttt cgtgaatggt ctccacccac ctgtgcctgg 989

cggacccact ctccagtagg gaggggcccgg gccatccctg acacgaagct ccttgggccc 1049

gtgaagtcac acatcgccctt ctcgccgtcc ccaccccctc catttggcag 1099

```
<210> 26
<211> 269
<212> PRT
<213> Homo sapiens
```

```
<400> 26
Met Ala His Leu Val Asn Ser Val Ser Asp Ile Leu Asp Ala Leu Gln
      1              5              10              15
```

Arg Asp Arg Gly Leu Gly Arg Pro Arg Asn Lys Ala Asp Leu Gln Arg
20 25 30

Ala Pro Ala Arg Gly Thr Arg Pro Arg Gly Cys Ala Thr Gly Ser Arg
35 40 45

Pro Arg Asp Cys Leu Asp Val Leu Leu Ser Gly Gln Gln Asp Asp Gly
50 55 60

54

[illegible]

170							175					180						
gca ggc gac tcc ctc ctg aag cac agc ggc atg agg ttc acc acc aag	631																	
Ala Gly Asp Ser Leu Leu Lys His Ser Gly Met Arg Phe Thr Thr Lys																		
185	190	195																
gac cgt gac agc gac cat tca gag aac aac tgt gcc gcc ttc tac cgc	679																	
Asp Arg Asp Ser Asp His Ser Glu Asn Asn Cys Ala Ala Phe Tyr Arg																		
200	205	210																
ggc gcc tgg tgg tac cgc aac tgc cac acg tcc aac ctc aat ggg cag	727																	
Gly Ala Trp Trp Tyr Arg Asn Cys His Thr Ser Asn Leu Asn Gly Gln																		
215	220	225	230															
tac ctg cgc ggt gcg cac gcc tcc tat gcc gac ggc gtg gag tgg tcc	775																	
Tyr Leu Arg Gly Ala His Ala Ser Tyr Ala Asp Gly Val Glu Trp Ser																		
235	240	245																
tcc tgg acc ggc tgg cag tac tca ctc aag ttc tct gag atg aag atc	823																	
Ser Trp Thr Gly Trp Gln Tyr Ser Leu Lys Phe Ser Glu Met Lys Ile																		
250	255	260																
cgg ccg gtc cgg gag gac cgc tagaccggtg caccttgtcc ttggccctgc	874																	
Arg Pro Val Arg Glu Asp Arg																		
265																		
tggtccctgt cgccccatcc ccgaccccac ctcaactcttt cgtgaatggt ctccaccac	934																	
ctgtgcctgg cggaccacact ctccagtagg gaggggcccgg gccatccctg acacgaagct	994																	
ccctggggccg gtgaagtcac acatgcgctt ctgcgcgtcc ccaccccctc catttggcag	1054																	

```
<210> 28
<211> 269
<212> PRT
<213> Homo sapiens
```

```
<400> 28
Met Ala His Leu Val Asn Ser Val Ser Asp Ile Leu Asp Ala Leu Gln
  1                      5                      10                      15
Arg Asp Arg Gly Leu Gly Arg Pro Arg Asn Lys Ala Asp Leu Gln Arg
          20                      25                      30
Ala Pro Ala Arg Gly Thr Arg Pro Arg Gly Cys Ala Thr Gly Ser Arg
      35                      40                      45
```


[illegible]

$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{x}} \right) = \frac{\partial L}{\partial x}$

<222> (1) .. (498)

atg aat ttt ctg aaa tta att gct gtg ttt ata gtt ttt agc cat gca	48
Met Asn Phe Leu Lys Leu Ile Ala Val Phe Ile Val Phe Ser His Ala	
1 5 10 15	
tcg gaa tca cct cag gac tcc act ccc aat caa tta tat atc tgg ggg	96
Ser Glu Ser Pro Gln Asp Ser Thr Pro Asn Gln Leu Tyr Ile Trp Gly	
20 25 30	
agg acc aag gcg ttg gta ttt ttc aga agc tcc act ggt gat tct gac	144
Arg Thr Lys Ala Leu Val Phe Phe Arg Ser Ser Thr Gly Asp Ser Asp	
35 40 45	
agc aca gct agg att aag aaa ctg atc aat ggg aac agc atg cct gtt	192
Ser Thr Ala Arg Ile Lys Lys Leu Ile Asn Gly Asn Ser Met Pro Val	
50 55 60	
gca gag gag ctt ccc tgg gaa atg tca cac aca gaa cat caa tct tcc	240
Ala Glu Glu Leu Pro Trp Glu Met Ser His Thr Glu His Gln Ser Ser	
65 70 75 80	
ttc ccc act cct gag atc cct cat tct ttg gca cca gga aca gtt gca	288
Phe Pro Thr Pro Glu Ile Pro His Ser Leu Ala Pro Gly Thr Val Ala	
85 90 95	
att agt aaa ccc tgg ttc cct gct gtc tca caa atc gca aga gtc caa	336
Ile Ser Lys Pro Trp Phe Pro Ala Val Ser Gln Ile Ala Arg Val Gln	
100 105 110	
cgt gtg gat ata aac ttt tgt tca tgg gag gat ctt tct ccc agt gga	384
Arg Val Asp Ile Asn Phe Cys Ser Trp Glu Asp Leu Ser Pro Ser Gly	
115 120 125	
aaa gca act ggg aaa agc agg aca cac tgc aca gtg act gca gtt tca	432
Lys Ala Thr Gly Lys Ser Arg Thr His Cys Thr Val Thr Ala Val Ser	
130 135 140	
tcc aat gcc acc acc cat gca ggc ata aat aat gaa cat gga tgg ggg	480
Ser Asn Ala Thr Thr His Ala Gly Ile Asn Asn Glu His Gly Trp Gly	
145 150 155 160	
agt ctg gag ctg ctg aat	498
Ser Leu Glu Leu Leu Asn	
165	

cagagagcgc ctgcccgggg aaccgcggcc cggggctgtg cactggctc ccggccccga 60

gactgtcttg acgtcctcct aagcggacag caggacgatg gcgctactc tgtctttccc 120

accactacc cggccggctt ccagggtgtac tgtgacatgc gcacggacgg cggcggctgg 180

acgggtgttc agcgcgggga ggacggctcc gtgaacttct tccggggctg ggacgcgtac 240

cgagacggct ttggcaggct caccggggag cactggctag ggctcaagag gatccacgcc 300

ctgaccacac aggctgccta cgagctgcac gtggacctg aggactttga gaatggcacg 360

gcctatgccc gctacgggag cttcggcggtg ggcttgttcg ccgtggacct tgaggaagac 420

gggtaccgc tcaccgtggc tgactattcc ggcatgcag gcgactccct cctgaagcac 480

agcggcatga ggttcaccac caaggaccgt gacagcgacc attcagagaa caactgtgcc 540

gccttctacc gcggtgcctg gtggtaccgc aactgccaca cgtccaacct caatgggcag 600

tacctgcgcg gtgcgcacgc ctctatgcc gacggcggtg agtggctctc ctggaccggc 660

tggcagtact cactcaagtt ctctgagatg aagatccggc cggtcgggga ggaccgc 717

<210> 32

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo Primer

<400> 32

ctcgtcctcg agggtaagcc tatccctaac

30

<210> 33

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo Primer

<400> 33

ctcgtcgggc ccctgatcag cggggtttaa c

31

<210> 34
 <211> 40
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligo Primer

 <400> 34
 ctcgtcagat ctcgcagcgg agatgccacc ttccccaaag 40

 <210> 35
 <211> 40
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligo Primer

 <400> 35
 ctcgtcctcg agcctcctcg acgtgccggt gctcacctcg 40

 <210> 36
 <211> 43
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligo Primer

 <400> 36
 ggatccacca tgaattttct gaaattaatt gctgtgttta tag 43

 <210> 37
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Oligo Primer

 <400> 37
 ctcgagattc agcagctcca gactccccca tccatg 36

(The following information was obtained from the above-mentioned sources.)

<210> 38

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo Primer

<400> 38

agatctcaga gagcgccctgc ccgggggaacc

30

<210> 39

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo Primer

<400> 39

ctcgaggcgg tcctcccgga ccggccggat c

31

<210> 40

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo Primer

<400> 40

gaggacggct ccgtgaac

18

<210> 41

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo Primer

<400> 41

gttcacggag ccgtcctc

18

<210> 42
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligo Primer

<400> 42
 cagcggcatg aggttcacc 19

<210> 43
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligo Primer

<400> 43
 ggtgaacctc atgccgctg 19

<210> 44
 <211> 14
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligo Primer

<400> 44
 catggtcagc ctac 14

<210> 45
 <211> 14
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligo Primer

<400> 45
 tcgagtaggc tgac 14

<210> 46
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo Primer

<400> 46

tccctgggaa atgtcacaca

20

<210> 47

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo Primer

<400> 47

ttcctgggtgc caaagaatga g

21

<210> 48

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo Primer

<400> 48

agaacatcaa tcttccttcc ccactcctga g

31

<210> 49

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo Primer

<400> 49

gcctggctct ctggatagac a

21

<220>

<400> 50

20

<220>

<400> 51

21

<220>

<400> 52

23

<220>

<400> 53

18

<210> 54
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligo Primer

<400> 54
 cctctttgtt cttcttgccc gagttttctt t 31

<210> 55
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligo Primer

<400> 55
 tggaagtcctc tcggtaaagg a 21

<210> 56
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligo Primer

<400> 56
 aggacacctg tgccctgtct 20

<210> 57
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Oligo Primer

<400> 57
 cccgccttgc cattcccttc a 21